

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 4, 2002, 07:41:05 ; Search time 15.04 Seconds
(without alignments)
2365.909 Million cell updates/sec

Title: US-08-153-397a-2
Perfect score: 4928
Sequence: 1 MGPEALSSLLLLLVASGDA.....ORPPFSQHLRLAEDALNTV 919

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SWISSProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4887	99.2	913	1	DDRL_HUMAN
2	4576.5	92.9	910	1	DDRL_RAT
3	4560	92.5	911	1	DDRL_MOUSE
4	2404	48.8	855	1	DDRL_MOUSE
5	2402	48.7	854	1	DDRL_MOUSE
6	648.5	13.2	821	1	TRKB_MOUSE
7	648.5	13.2	821	1	TRKB_MOUSE
8	648	13.1	818	1	TRKB_MOUSE
9	645	13.1	822	1	TRKB_MOUSE
10	642	13.0	796	1	TRKA_MOUSE
11	640.5	13.0	799	1	TRKA_MOUSE
12	636.5	12.9	778	1	TRKA_MOUSE
13	626.5	12.7	827	1	TRKC_MOUSE
14	624.5	12.7	825	1	TRKC_MOUSE
15	623.5	12.7	839	1	TRKC_MOUSE
16	596	12.1	605	1	TRKC_MOUSE
17	590.5	12.0	604	1	TRKC_MOUSE
18	540.5	11.0	1363	1	TRKC_MOUSE
19	540	11.0	937	1	TRKB_MOUSE
20	537	10.9	937	1	TRKB_MOUSE
21	535.5	10.9	1382	1	INSR_MOUSE
22	532.5	10.8	402	1	INSR_MOUSE
23	532.5	10.8	507	1	INSR_MOUSE
24	531.5	10.8	1372	1	INSR_MOUSE
25	528.5	10.7	1383	1	INSR_MOUSE
26	523	10.6	1520	1	ABLI_MOUSE
27	523	10.6	2347	1	ABLI_MOUSE
28	520	10.6	794	1	TRK1_MOUSE
29	520	10.6	746	1	TRK1_MOUSE
30	520	10.6	1123	1	ABLI_MOUSE
31	517	10.5	1130	1	ABLI_MOUSE
32	517	10.5	1300	1	IRK_MOUSE
33	515	10.5	943	1	ROR2_MOUSE

34	514	10.4	439	1	ABLI_MOUSE
35	513	10.4	1287	1	IRK_MOUSE
36	513	10.4	2594	1	IRK_MOUSE
37	510.5	10.4	1379	1	IRK_MOUSE
38	508.5	10.3	1390	1	IRK_MOUSE
39	508	10.3	1382	1	IRK_MOUSE
40	508	10.3	1387	1	IRK_MOUSE
41	508	10.3	2146	1	IRK_MOUSE
42	506	10.3	640	1	IRK_MOUSE
43	506	10.3	944	1	IRK_MOUSE
44	505.5	10.3	1382	1	IRK_MOUSE
45	500.5	10.2	1373	1	IRK_MOUSE

ALIGNMENTS

RESULT	ID	STANDARD	PRT	913 AA.
1	DDRL_HUMAN	008345; 014196; Q16562;		
2	DDRL_HUMAN	01-FEB-1995 (Rel. 31, Created)		
3	DDRL_HUMAN	01-NOV-1997 (Rel. 35, Last sequence update)		
4	DDRL_HUMAN	01-MAR-2002 (Rel. 41, Last annotation update)		
5	DDRL_HUMAN	Epithelial discoidin domain receptor 1 precursor (EC 2.7.1.112)		
6	DDRL_HUMAN	(Tyrosine-protein kinase Cdk) (Cell adhesion kinase) (Tyrosine kinase)		
7	DDRL_HUMAN	(Tyrosine-protein kinase Cdk) (Cell adhesion kinase) (Tyrosine kinase)		
8	DDRL_HUMAN	(Tyrosine-protein kinase Cdk) (Cell adhesion kinase) (Tyrosine kinase)		
9	DDRL_HUMAN	(Tyrosine-protein kinase Cdk) (Cell adhesion kinase) (Tyrosine kinase)		
10	DDRL_HUMAN	(Tyrosine-protein kinase Cdk) (Cell adhesion kinase) (Tyrosine kinase)		
11	DDRL_HUMAN	(Tyrosine-protein kinase Cdk) (Cell adhesion kinase) (Tyrosine kinase)		
12	DDRL_HUMAN	(Tyrosine-protein kinase Cdk) (Cell adhesion kinase) (Tyrosine kinase)		
13	DDRL_HUMAN	(Tyrosine-protein kinase Cdk) (Cell adhesion kinase) (Tyrosine kinase)		
14	DDRL_HUMAN	(Tyrosine-protein kinase Cdk) (Cell adhesion kinase) (Tyrosine kinase)		
15	DDRL_HUMAN	(Tyrosine-protein kinase Cdk) (Cell adhesion kinase) (Tyrosine kinase)		
16	DDRL_HUMAN	(Tyrosine-protein kinase Cdk) (Cell adhesion kinase) (Tyrosine kinase)		
17	DDRL_HUMAN	(Tyrosine-protein kinase Cdk) (Cell adhesion kinase) (Tyrosine kinase)		
18	DDRL_HUMAN	(Tyrosine-protein kinase Cdk) (Cell adhesion kinase) (Tyrosine kinase)		
19	DDRL_HUMAN	(Tyrosine-protein kinase Cdk) (Cell adhesion kinase) (Tyrosine kinase)		
20	DDRL_HUMAN	(Tyrosine-protein kinase Cdk) (Cell adhesion kinase) (Tyrosine kinase)		
21	DDRL_HUMAN	(Tyrosine-protein kinase Cdk) (Cell adhesion kinase) (Tyrosine kinase)		
22	DDRL_HUMAN	(Tyrosine-protein kinase Cdk) (Cell adhesion kinase) (Tyrosine kinase)		
23	DDRL_HUMAN	(Tyrosine-protein kinase Cdk) (Cell adhesion kinase) (Tyrosine kinase)		
24	DDRL_HUMAN	(Tyrosine-protein kinase Cdk) (Cell adhesion kinase) (Tyrosine kinase)		
25	DDRL_HUMAN	(Tyrosine-protein kinase Cdk) (Cell adhesion kinase) (Tyrosine kinase)		
26	DDRL_HUMAN	(Tyrosine-protein kinase Cdk) (Cell adhesion kinase) (Tyrosine kinase)		
27	DDRL_HUMAN	(Tyrosine-protein kinase Cdk) (Cell adhesion kinase) (Tyrosine kinase)		
28	DDRL_HUMAN	(Tyrosine-protein kinase Cdk) (Cell adhesion kinase) (Tyrosine kinase)		
29	DDRL_HUMAN	(Tyrosine-protein kinase Cdk) (Cell adhesion kinase) (Tyrosine kinase)		
30	DDRL_HUMAN	(Tyrosine-protein kinase Cdk) (Cell adhesion kinase) (Tyrosine kinase)		
31	DDRL_HUMAN	(Tyrosine-protein kinase Cdk) (Cell adhesion kinase) (Tyrosine kinase)		
32	DDRL_HUMAN	(Tyrosine-protein kinase Cdk) (Cell adhesion kinase) (Tyrosine kinase)		
33	DDRL_HUMAN	(Tyrosine-protein kinase Cdk) (Cell adhesion kinase) (Tyrosine kinase)		

RP SEQUENCE FROM N.A. (SHORT FORM).
 RC TISSUE-BRAIN, and Keratinocytes;
 RX MEDLINE=94043265; PubMed=8226977;
 RA "di Marco E., Cutuli N., Guerra L., Cancedda R., de Luca M.,
 RT "Molecular cloning of tkrx, a novel tkr-related putative tyrosine
 RT kinase receptor isolated from normal human keratinocytes and widely
 RT expressed by normal human tissues.";
 RL J. Biol. Chem. 268:24290-24295(1993).
 RM [7]
 RP SEQUENCE FROM N.A. (SHORT FORM).
 RC TISSUE-Ovary;
 RX MEDLINE=93151638; PubMed=7848919;
 RA Laval S., Butler R., Shelling A.N., Hanby A.M., Poulson R.,
 RT Ganesan T.S.;
 RT "Isolation and characterization of an epithelial-specific receptor
 RT tyrosine kinase from an ovarian cancer cell line.";
 RL Cell Growth Differ. 5:1173-1183(1994).
 RM [8]
 RP SEQUENCE FROM N.A.
 RA Shilina S., Tamiya G., Oka A., Inoko H.;
 RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MAY BE INVOLVED IN CELL-CELL INTERACTIONS AND
 CC RECOGNITION.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOPFORMS: 1/CAK I (SHOWN HERE) AND 2/CAK
 CC II; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ONLY DIFFER BY THE
 CC ABSENCE OF A 37 RESIDUES SEGMENT.
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT LOW LEVELS IN MOST ADULT TISSUES
 CC AND IS HIGHEST IN THE BRAIN AND LUNG. ABUNDANT IN BREAST CARCINOMA
 CC CELL LINES.
 CC -1- DOMAIN: THE GLY/PRO-RICH DOMAINS MAY BE REQUIRED FOR AN UNUSUAL
 CC GEOMETRY OF INTERACTION WITH LIGAND OR SUBSTRATES.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 CC -1- DATABASE: NAME=PRO; NOTE=CD guide CD167a entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/1986613159_g.htm".
 CC -----
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 CC -----
 DR EMBL; L11315; AAA02866.1; -;
 DR EMBL; L20817; AAA18019.1; -;
 DR EMBL; U48705; AAC50917.1; -;
 DR EMBL; X98208; CAA66871.1; -;
 DR EMBL; X99023; CAA66871.1; JOINED.
 DR EMBL; X99024; CAA66871.1; JOINED.
 DR EMBL; X99025; CAA66871.1; JOINED.
 DR EMBL; X99026; CAA66871.1; JOINED.
 DR EMBL; X99027; CAA66871.1; JOINED.
 DR EMBL; X99028; CAA66871.1; JOINED.
 DR EMBL; X99029; CAA66871.1; JOINED.
 DR EMBL; X99030; CAA66871.1; JOINED.
 DR EMBL; X99031; CAA66871.1; JOINED.
 DR EMBL; X99032; CAA66871.1; JOINED.
 DR EMBL; X99033; CAA66871.1; JOINED.
 DR EMBL; X99034; CAA66871.1; JOINED.
 DR EMBL; L57508; AAB05208.1; -;
 DR EMBL; X74979; CAA52915.1; -;
 DR EMBL; X29093; CAA82335.1; -;
 DR EMBL; AP000511; BAB63318.1; -;
 DR HSP; P11362; JFGK.
 DR MIM; 600408; -;

DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR000421; FAS8_C.
 DR InterPro: IPR000211; Receptor_tyr_kin_II.
 DR InterPro: IPR001245; Tyr_Pkinase.
 DR Pfam: PF00734; F5_F8_type_C; 1.
 DR Pfam: PF00069; Pkinase; 1.
 DR SMART: SM00231; FAS8C; 1.
 DR SMART: SM00219; TyrKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP_FALSE_NEG.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
 DR PROSITE: PS01285; FAS8C_1; 1.
 DR PROSITE: PS01286; FAS8C_2; 1.
 KW Transferrase: Tyrosine-protein kinase; Glycoprotein; Signal;
 KW Phosphorylation; Transmembrane; Receptor; ATP-binding; Antigen;
 KW Alternative splicing.
 KW SIGNAL 1 18
 FT CHAIN 19 913
 FT DOMAIN 19 416
 FT TRANSMEM 417 443
 FT DOMAIN 444 913
 FT DOMAIN 31 185
 FT DOMAIN 377 415
 FT DOMAIN 476 601
 FT DOMAIN 610 905
 FT NP_BIND 616 624
 FT BINDING 655 655
 FT ACT_SITE 766 766
 FT DISULFID 31 185
 FT MOD_RES 513 513
 FT MOD_RES 792 792
 FT MOD_RES 796 796
 FT MOD_RES 797 797
 FT CARBOHYD 211 211
 FT CARBOHYD 260 260
 FT CARBOHYD 371 371
 FT CARBOHYD 394 394
 FT VARSPLIC 506 542
 FT CONFLICT 94 94
 FT CONFLICT 833 833
 FT CONFLICT 847 867
 FT
 SQ SEQUENCE 913 AA: 101127 MW: C96913EA906C481E CRC64:
 Query Match 99.2%; Score 4887; DB 1; Length 913;
 Best Local Similarity 99.3%; Pred. No. 7; le-251;
 Matches 913; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
 QY 1 MGPEALSSLLLLLVASGDADMKGHFPAKCRYALGMODRTIPSDISASSMSDSTAR 60
 DB 1 MGPEALSSLLLLLVASGDADMKGHFPAKCRYALGMODRTIPSDISASSMSDSTAR 60
 QY 61 HSRLESSDGDAMCPAGSVFPEKEEYLOVDLQRLHLVALVGTQGHAGCLKEFSRSL 120
 DB 61 HSRLESSDGDAMCPAGSVFPEKEEYLOVDLQRLHLVALVGTQGHAGCLKEFSRSL 120
 QY 121 RYSRDGRMRMGKMRMGQEVISGNEDPEGVYLKDLGPPMVARLVFYRRADRVMSVCRLV 180
 DB 121 RYSRDGRMRMGKMRMGQEVISGNEDPEGVYLKDLGPPMVARLVFYRRADRVMSVCRLV 180
 QY 181 ELYCGLMRDGLLSTAPVGGTMYLSEAVYLLNDSTYDGHVTGGLGYGGLGADGVGGLD 240
 DB 181 ELYCGLMRDGLLSTAPVGGTMYLSEAVYLLNDSTYDGHVTGGLGYGGLGADGVGGLD 240
 QY 241 FRKSOELRWMPGVYVGSNSHSSGVYEMFEEDRLRAPAMOVHCHNMHTLGLARLPGG 300
 DB 241 FRKSOELRWMPGVYVGSNSHSSGVYEMFEEDRLRAPAMOVHCHNMHTLGLARLPGG 300
 QY 301 VECRRRGAPAMAWGGEPRRHNLGNNLGPARRAASVPLGGRVAFLLCRLFLAGPMLLFS 360
 DB 301 VECRRRGAPAMAWGGEPRRHNLGNNLGPARRAASVPLGGRVAFLLCRLFLAGPMLLFS 360

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Db 301 VECFRRCBPAMWEGEPHNLGNLGDPRARAVSYPLGGVARFLQCRFLFAGPMLIFS 360
QY 361 ELSFISDVYNNSSPALGSGFPFPPMPMPPPPPPPPPPPPPPPPPPPPPPPPPPP 420
Db 361 ELSFISDVYNNSSPALGSGFPFPPMPMPPPPPPPPPPPPPPPPPPPPPPPPPPP 420
QY 421 GCLVAIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII 480
Db 421 GCLVAIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII 480
QY 481 PPPYQEPFRGNPPHSPAPCVNPGSALLSNPAYRLLATYARPGRPPPTPMAKPNT 540
Db 481 PPPYQEPFRGNPPHSPAPCVNPGSALLSNPAYRLLATYARPGRPPPTPMAKPNT 540
QY 541 QAYSGDYMEPEKPGAPLLPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 600
Db 541 QAYSGDYMEPEKPGAPLLPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 600
QY 601 PRVDEPRSRRLRFRKEKLEGEQFGEVHLCEVDSPODLVSLDFPLVRKGPPLVAVKILRPD 660
Db 601 PRVDEPRSRRLRFRKEKLEGEQFGEVHLCEVDSPODLVSLDFPLVRKGPPLVAVKILRPD 660
QY 661 ATKNSFSLSSRNDFLEKVKIMSRLKDPNIIIRLLGVCVDDPLCMITDYMENGLNQFLS 720
Db 661 ATKNSFSLSSRNDFLEKVKIMSRLKDPNIIIRLLGVCVDDPLCMITDYMENGLNQFLS 720
QY 721 AQLQEDKAAEGAPGQQAAGPTISYPMILHYAAQASGRIATLNFYHRIATNCLV 780
Db 721 AQLQEDKAAEGAPGQQAAGPTISYPMILHYAAQASGRIATLNFYHRIATNCLV 780
QY 781 GENFTIKIDFGMSRLVAGDYRYVGRVAVLPPIRMWAMECILMGKFTTASDWAFCVTLM 840
Db 781 GENFTIKIDFGMSRLVAGDYRYVGRVAVLPPIRMWAMECILMGKFTTASDWAFCVTLM 840
QY 841 EYLMICRAQPFQGLTDEQYIENAGFEFFRDQGRQVYLSRPACPOGLIYELMLRCMSRESE 900
Db 841 EYLMICRAQPFQGLTDEQYIENAGFEFFRDQGRQVYLSRPACPOGLIYELMLRCMSRESE 900
QY 901 RPPFSQLHFLAEDALNTY 919
Db 901 RPPFSQLHFLAEDALNTY 919
QY 919 RPPFSQLHFLAEDALNTY 919
Db 919 RPPFSQLHFLAEDALNTY 919

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CC -1- TISSUE SPECIFICITY: VARIOUS EMBRYONIC AND ADULT TISSUES; ALSO
CC PROLIFERATIVE ZONES OF THE DEVELOPING BRAIN; HIPPOCAMPAL NEURONS.
CC -1- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF TYR-PROTEIN
CC KINASES.
CC -1- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -----
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CC or send an email to license@sdb.ch).
CC -----
CC EMBL: L26525; AAA21089.1; -.
CC HSSP: P1362; IAGW.
CC DR InterPro: IPR000719; Euk_pkinase.
CC DR InterPro: IPR000421; FAS8_C.
CC DR InterPro: IPR002011; Receptor_tyr_kin_II.
CC DR InterPro: IPR001245; Tyr_pkinase.
CC DR Pfam: PF00754; F5_F8_type_C.1.
CC DR Pfam: PF00069; pkinase.1.
CC DR SMART: SM00231; FAS8C.1.
CC DR SMART: SM00219; Tyrc.1.
CC DR PROSITE: PS00109; PROTEIN_KINASE_TYR.1.
CC DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II.1.
CC DR PROSITE: PS01285; FAS8C.1.1.
CC DR PROSITE: PS01286; FAS8C.2.1.
CC DR PROSITE: PS00011; PROTEIN_KINASE_DOM.1.
CC DR Transferrase: Tyrosine-protein kinase; Glycoprotein; signal;
CC KW phosphorylation; Transmembrane; Receptor; ATP-binding.
CC FT SIGNAL 1 19
CC FT CHAIN 20 910
CC FT DOMAIN 20 413
CC FT TRANSMEM 414 440
CC FT DOMAIN 441 910
CC FT DOMAIN 32 186
CC FT FT 378 412
CC FT FT 473 598
CC FT DOMAIN 607 902
CC FT NP_BIND 613 621
CC FT BINDING 652 652
CC FT ACT_SITE 763 763
CC FT DISULFID 32 186
CC FT MOD_RES 510 510
CC FT MOD_RES 789 789
CC FT MOD_RES 793 793
CC FT MOD_RES 794 794
CC FT CARBOHYD 212 212
CC FT CARBOHYD 261 261
CC FT CARBOHYD 371 371
CC FT CARBOHYD 391 391
CC FT SEQUENCE 910 AA: 101164 MW: 767FAIDDB029806 CRC64;

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Query Match 92.9%; Score 4576.5; DB 1; Length 910;
Best Local Similarity 93.0%; Pred. No. 1.7e-234;
Matches 856; Conservative 20; Mismatches 33; Indels 11; Gaps 3;

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KM Transferase; Tyrosine-protein kinase; Glycoprotein; Signal;
 KM Phosphorylation; Transmembrane; Receptor; ATP-binding.
 FT SIGNAL 1 21
 FT CHAIN 22 855
 FT DOMAIN 22 399
 FT TRANSHEM 400 421
 FT DOMAIN 422 855
 FT DOMAIN 30 185
 FT DOMAIN 563 849
 FT NP_BIND 569 577
 FT BINDING 608 608
 FT ACT_SITE 710 710
 FT DISULFID 30 185
 FT MOD_RES 740 740
 FT CARBOHYD 121 121
 FT CARBOHYD 213 213
 FT CARBOHYD 261 261
 FT CARBOHYD 280 280
 FT CARBOHYD 372 372
 FT SEQUENCE 855 AA; 96752 MW; D5270BCCFD7FED7E CRC64;
 SO
 Query Match 48.88; Score 2404; DB 1; Length 855;
 Best Local Similarity 51.88; Pred. No. 5.9e-120;
 Matches 482; Conservative 118; Mismatches 227; Indels 104; Gaps 16;
 QY 3 PEALSLILLLVASGDADMGHPDPAKCRALGMQDRTIPDSISASSWSSTARS 62
 DB 5 PMLVLFLLPLLS---SAKAQVNPALCRPLGMSGQIDDEDITASSQSESTAA 61
 QY 63 RLSSDGDGACMPAGSVFPEKE-EETVQVLDLRLHLVALVGTGGHAGLGKFSRYLR 121
 DB 62 RLDSSEGGACMPCEIPVPPDLEKELQIDLHTLHITLVGTGGHAGHIEFAPMYKIN 121
 QY 122 YSPGRRMGKMDKRGQVIGSNGDEBEGVVLKDGPRVAVLVPRADVMSCLEAVE 181
 DB 122 YSRDSTIRISNRKRGKVLGNSNPDIKLEPPVIAFVPRIPYTDHSMVNCMEVE 181
 QY 182 LYGLMDRLGLSYTAPVQGTMYL--SEAVYLNDSTYDGTGGLQYGGIQLADGVVLD 239
 DB 182 LYGCWMDGLVSYNAPAGQGVLPGGSTIYLNDVYDQ-ANGYMTBELGGLTGCVSLD 240
 QY 240 DFRSQELRVPGIDYGVSMHSSSGVTEMEFEFRLRAFOAMOVHNNHTLGARLP 299
 DB 241 DFTQHEHVMPGYDYGVWRNESATNGIETIMFEFDIRINFTYAKVHNNFAKGVKLEK 300
 QY 300 GVECFRRGPMAMEGEMRNHNGNLGDPRAVASVGLGRVAFLOCRLFAQWLLF 359
 DB 301 EVOCTF-RSEASEWEPNALSFPVLVDVNSARFVTVPLHHRMASAIKCOYFADTWMF 359
 QY 360 SEISFISD-VVNSSPALGTFPPAPWMPGPPTNFSLELEPRGOQPVAKAGSPYAI 418
 DB 360 SEIFQSDAAMYNSEAL---PTSP-----MAPTYDPMKAVDQSNRI 400
 QY 419 LIGCLVALIILLLIILALMLRLRLLSKAERVLLEELTVLSPVGGTILNNR-P 476
 DB 401 LIGCLVALIILLLIILALMLRLRLLSKAERVLLEELTVLSPVGGTILNNR-P 476
 QY 477 GPREP-----PRYOEPGRGNPNPHSAPCVNGSALLSNPAYLLATYAR 523
 DB 461 SPSSQGSSTYDRIFPLPDIQEP-----SRLTRKLEP----- 494
 QY 524 PRGPGPTPAMAKPTNTQAVSGDYMEEKPGAPLLPPPPONSVHYAEADIVTLQGVG 583
 DB 495 -----APGEESGSGSVYKVPQSGP-----EGVHYAEADIVNLQGVG 535
 QY 584 NTYAVPALPRAVGDGPRV-DPRSRRLRREKIGESQFGVHLCEVDSPQDLVSLDFPL 642
 DB 536 NTYSPVATMDLISGKDVAAVEEPRKILTEFEKIGESQFGVHLCEVEGMEKFKDQFAL 595
 QY 643 NVRGHPLLVAVKITLRPDATKNASFLSRNDELKEVKINSRLKDPNITIRLGCYQDDP 702
 DB 596 DVSANQVLAVALKLRADANKA-----RNDPLKEIKIRSLKDPNITIRLGCYQDDP 649

QY 703 LCMITDYENGDLNLOFLSAHQLEDKACAGAPDGOAGOPTISYPMILHVAQIASGRY 762
 DB 650 LCMITEYENGDLNLOFLSRHE-----PNNSSSDVRYSTYMLFMATQIASGRY 700
 QY 763 LATNFVRDLATRNCLVGENFTIKIADFGMSRNLYAGDYRVQRAVLPIRMAMECIL 822
 DB 701 LSLNLFVRDLATRNCLVGENFTIKIADFGMSRNLYAGDYRVQRAVLPIRMAMECIL 760
 QY 823 MGFETTADVAFGYTLWEVLMCRAPFGQITDEQVLENAGEFFRDGROYLSRPPAC 882
 DB 761 LKFTTADVAFGYTLWEVLMCRAPFGQITDEQVLENAGEFFRDGROYLSRPPAC 820
 QY 883 POGYEMLRCMSRESEORPPESOLHRELA 913
 DB 821 PDSYKMLSCWRDTPKRPSEOEIHLILLO 851
 RESULT 5
 DDB2_MOUSE
 ID DDB2_MOUSE STANDARD; PRT: 854 AA.
 AC 062371.
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Discoidin domain receptor 2 precursor (BC 2.7.1.112) (Receptor
 DE protein-tyrosine kinase TKT) (Tyrosine-protein kinase TYRO 10)
 DE (Neurotrophic tyrosine kinase; receptor-related 3).
 GN DDB2 OR NTKR3 OR TKT OR TYRO10.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RX [1]
 RP SEQUENCE FROM N. A.
 RX MEDLINE=94067796; PubMed=8247548;
 RA Kan T., Holtrich U., Braeuninger A., Boehme B., Wolf G.,
 RA Rubsamen-Waigmann H., Strebhardt K.;
 RT "Structure, expression and chromosomal mapping of TKT from man and
 RT mouse: a new subclass of receptor tyrosine kinases with a factor
 RT VIII-like domain.";
 RL Oncogene 8:3433-3440(1993).
 RP [2]
 RP SEQUENCE FROM N. A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=94151011; PubMed=8108131;
 RA Lal C., Lemke G.E.;
 RT "Structure and expression of the Tyro 10 receptor tyrosine kinase.";
 RL Oncogene 9:877-883(1994).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: DIFFERENT TRANSCRIPTS ARE DERIVED FROM ONE
 CC GENE.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED; HIGH LEVELS IN SKELETAL
 CC MUSCLE, HEART, CNS, AND KIDNEY; LESS IN OTHER TISSUES. THE MAJOR
 CC 10 KDa TRANSCRIPT IS EXPRESSED IN HIGH LEVELS IN HEART AND LUNG,
 CC LESS IN BRAIN AND TESTIS.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
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 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC EMBL; X76505; CAA54040.1; ALT_INIT.

DB 747 TYRK-OPWOLSNNEVEICT-----TQGR-VLORPRTCPQEVYELMGCGQRPHPRKX 798
 OY 904 FSQHLNRL 911
 DB 799 IKSHITLL 806

RESULT 7
 TRKB_RAT STANDARD: PRT: 821 AA.
 AC 063604: 063605: 063606:
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE BDNF/NT-3 growth factors precursor (EC 2.7.1.112) (TRKB
 tyrosine kinase) (GPI45-TRKB/GP95-TRKB) (Trk-B).
 GN NTRK2 OR TRKB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid-10116;
 RN [1]
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
 RC TISSUE-Cerebellum;
 RX MEDLINE-91094826; PubMed-1846020;
 RA Middlemas D.S., Lindberg R.A., Hunter T.;
 RT "trkb, a neural receptor protein-tyrosine kinase: evidence for a
 full-length and two truncated receptors";
 RL Mol. Cell. Biol. 11:143-153(1991).
 RN [2]
 RP PHOSPHORYLATION SITES.
 RX MEDLINE-94149017; PubMed-8106527;
 RA Middlemas D.S., Meisenhelder J., Hunter T.;
 RT "Identification of Trkb autophosphorylation sites and evidence that
 phospholipase C gamma 1 is a substrate of the Trkb receptor";
 RL J. Biol. Chem. 269:5458-5466(1994).
 CC -1- FUNCTION: RECEPTOR FOR BRAIN-DERIVED NEUROTROPHIC FACTOR (BDNF),
 NEUROTROPHIN-3 AND NEUROTROPHIN-4/5 BUT NOT NERVE GROWTH FACTOR
 (NGF). INVOLVED IN THE DEVELOPMENT AND/OR MAINTENANCE OF THE
 NERVOUS SYSTEM. THIS IS A TYROSINE-PROTEIN KINASE RECEPTOR. KNOWN
 SUBSTRATES FOR THE TRK RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-
 GAMMA-1.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
 tyrosine phosphate.
 CC -1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
 AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS: GPI45-TRKB (SHOWN
 HERE), T1/GP95-TRKB AND T2; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: THE DIFFERENT FORMS ARE DIFFERENTIALLY
 EXPRESSED IN VARIOUS CELL TYPES. THE T2 ISOFORM IS PRIMARILY
 EXPRESSED IN NEURONS.
 CC -1- PIM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.
 CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
 PROTEIN KINASES. TRK-TYPE SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL: M55291: AAA42279.1: -
 DR EMBL: M55292: AAA42280.1: -
 DR EMBL: M55293: AAA42281.1: -
 DR HSSP: P11362; IAGW.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR000372; LRR_Nterm.
 DR InterPro: IPR002011; Receptor_tyr_kin_II.
 DR InterPro: IPR001245; Tyr_Pkinase.
 DR Pfam: PF00047; Ig_1.
 DR Pfam: PF00560; LRR_1.
 DR Pfam: PF01463; LRRCT_1.
 DR Pfam: PF01462; LRRNT_1.
 DR Pfam: PF00069; Pkinase_1.
 DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00408; IGC2_1.
 DR SMART: SM00082; LRCT_1.
 DR SMART: SM00013; LRRNT_1.
 DR SMART: SM00219; TYRK_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
 DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM_1.
 DR Transferrase: Tyrosine-protein kinase; Transmembrane; ATP-binding;
 KW Phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;
 KW Leucine-rich repeat; Repeat; Immunoglobulin domain;
 KW Alternative splicing.
 FT SIGNAL 1 31
 FT CHAIN 32 821
 FT DOMAIN 32 429
 FT TRANSMEM 430 453
 FT DOMAIN 454 821
 FT REPEAT 72 93
 FT REPEAT 96 117
 FT DOMAIN 214 270
 FT DOMAIN 301 365
 FT DOMAIN 537 806
 FT NP_BIND 543 551
 FT BINDING 571 571
 FT ACT_SITE 675 675
 FT MOD_RES 515 515
 FT MOD_RES 701 701
 FT MOD_RES 705 705
 FT MOD_RES 706 706
 FT MOD_RES 816 816
 FT SITE 515 515
 FT SITE 816 816
 FT CARBOHD 67 67
 FT CARBOHD 95 95
 FT CARBOHD 121 121
 FT CARBOHD 178 178
 FT CARBOHD 205 205
 FT CARBOHD 241 241
 FT CARBOHD 254 254
 FT CARBOHD 280 280
 FT CARBOHD 325 325
 FT CARBOHD 338 338
 FT CARBOHD 411 411
 FT CARBOHD 411 411
 FT VARSPLIC 466 476
 FT VARSPLIC 477 821
 FT VARSPLIC 466 474
 FT VARSPLIC 475 821
 FT SEQUENCE 821 AA; 92186 MW; 0DDACCA212CDAA0E CRC64;
 SO

Query Match 13.2%; Score 648.5; DB 1; Length 821;
 Best Local Similarity 30.1%; Pred. No. 2,1e-27;
 Matches 201; Conservativity 72; Mismatches 188; Indels 207; Gaps 23;
 OY 373 SPALGCTPPAPMPPGPPPTFSSLEPRGQGVAAAGSPFVAILGCLVAITLLLL 432
 DB 217 SCSSGGDFPLTYLMDVGNLVSKHNNETSHQTGSLRITNMISSDDSGKQISCV----- 267

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OY 433 ITALMLRLMRLLSKARRVLEELVYHLSV---PGDTILINRPGPREP----- 482
DB 268 -----XENLVGEDODSDNVLVHFAPIITFL-----ESPSTDHMC 302
OY 483 -PYGEPFRGNPSPAPCPVNGS-----ALLSNNA-----Y 513
DB 303 IFF---TYRGNKPKALQWNYCAIINESKYICTKHVTNHNEYHCLDLQDNTNNGDY 359
OY 514 RLLI-----ATYARPPRGPPPTAMAKPTNTQAYSGDYMER--E 551
DB 360 TLMANEXGKDEROISAHFMGRPGVDYETNPVPEVLWEDMTPTDI---GDTINKSE 415
OY 552 KRGALLPPPPONSPHYAADIYTLQV-----580
DB 416 IPSTVDADQTNKHELSYAVVYASVGFCLVMLLLKLARSKFKGKSPASVISND 475
OY 581 -----TSGNTYAVVAPALPPGAVGDP---PRYDFP-----RS 608
DB 476 SASPLHISNGSNTPSSSEGGPDVAITGMTKIPYEENQYEGITNSQLKPDFTVOHIRH 535
OY 609 RLREKELGEGQFGEVHLCE---VDSPODLVSLDFPLNVRKGHPLLVAVKILRPDATRNA 665
DB 536 NVLKRRELGEGAFKVFIAECYNLCPEOD-----KLVAVKTLK-DASDA 580
OY 666 SFSLESRNDPLKEVKYIMRLDPNTRILGYCVODDPLCATTDIENGDLNOFLSAHOLE 725
DB 581 -----RQDFHREALLQHEHIVKRYGVCVEGDPIMVEFYKRDHLKFLAHPGD 634
OY 726 D-KAEGAPGQGAQGP--ISYPMILHVAQAQIASGMRYLATLNVHVDLATRNCLVGEN 783
DB 635 AVLAHEGMP-----PTELTOSOMLHIAQIAGVYLAHQHVDLHDLATRNCLVGEN 686
OY 784 FTIKIADGSMRLVAGDYRYRQRAVLPIRMMAECILMKFTYASDVMAFGVTLWEVL 843
DB 687 LLVKGDFGMSRDYVSTDYRYVGGHTMLPIRMPEESIMYKFTESVMSGLVYLMETIF 746
OY 844 MLCRAQPPGQULTDEQVYNAGEFFPDGROVYLSPPACPOGLYELMLRCSRESEQRP 903
DB 747 TYGK-RFLYQLSNNEVICI-----TQGR--VLARPRFCQEVYELMGCQREPHTRKN 798
OY 904 FSOLHRL 911
DB 799 IKNHTLL 806

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RT "Expression and binding characteristics of the BDNF receptor chick
trkB."
RL Development 119:545-558(1993).
CC -1- FUNCTION: RECEPTOR FOR BRAIN-DERIVED NEUROTROPHIC FACTOR (BDNF),
CC NEUROTROPHIN-3 AND NEUROTROPHIN-4/5 BUT NOT NERVE GROWTH FACTOR
CC (NGF). INVOLVED IN THE DEVELOPMENT AND/OR MAINTENANCE OF THE
CC NERVOUS SYSTEM. THIS IS A TYROSINE-PROTEIN KINASE RECEPTOR. KNOWN
CC SUBSTRATES FOR THE TRK RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-
CC GAMMA-1 (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine -> ADP + protein
CC tyrosine phosphate.
CC -1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
CC AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: A TRUNCATED NON-CATALYTIC FORM WHICH
CC FUNCTION REMAINS STILL UNCLEAR IS PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES. TRK-TYPE SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC
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CC or send an email to license@sib.ch).
CC
CC EMBL: X77251; CA54468.1; -
CC EMBL: X77252; CA54469.1; -
CC EMBL: X74109; CA52210.1; -
CC HSSP: P11362; IFG1.
CC InterPro: IPR000719; Euk_Pkinase.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003598; Ig_C2.
CC InterPro: IPR001611; LRR.
CC InterPro: IPR000483; LRR_Cterm.
CC InterPro: IPR000372; LRR_Nterm.
CC InterPro: IPR002011; Receptor_tyros_kin_II.
CC InterPro: IPR001245; Tyr_Pkinase.
CC Pfam: PF00047; Ig_1.
CC Pfam: PF00560; LRR_1.
CC Pfam: PF01463; LRCT; 1.
CC Pfam: PF00069; Pkinase; 1.
CC PRINTS: PR00109; TYRKINASE.
CC SMART: SM00408; IGC2; 1.
CC SMART: SM00082; LRCT; 1.
CC SMART: SM00013; LRRT; 1.
CC SMART: SM00219; TYKC; 1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
CC PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
CC PROSITE: PS50011; PROTEIN_KINASE_DOM_1.
CC PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
CC Transferrase: Tyrosine-protein kinase: transmembrane; ATP-binding;
CC phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;
CC Leucine-rich repeat; Repeat; Alternative splicing;
CC Immunoglobulin domain.
CC FT SIGNAL 1 31
CC FT CHAIN 32 818
CC FT DOMAIN 32 426
CC FT TRANSLEM 427 450
CC FT DOMAIN 451 818
CC FT REPEAT 95 92
CC FT DOMAIN 213 269
CC FT DOMAIN 300 364
CC FT DOMAIN 534 803
CC FT NP_BIND 540 548
CC FT BINDING 568 568
CC FT ACT_SITE 672 672

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FT MOD_RES 512 512 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 698 698 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 702 702 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 703 703 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 813 813 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT SITE 512 512 INTERACTION WITH SHC PROTEIN (BY SIMILARITY).
FT SITE 813 813 INTERACTION WITH PLC-GAMMA-1 (BY SIMILARITY).
FT CARBOHYD 66 66 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 94 94 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 120 120 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 204 204 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 226 226 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 324 324 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 337 337 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 408 408 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARSPIC 462 520 GRSVTSNDSDASPLHHSNGSTSSSGGPDVAVIIGT KIPVIEPQYFGITNSQL -> VHGKVGGLVDQIWLISQ DCDDNEQVATVNSDVHNNSTASDNNRGLGFVLFKIPLDG (IN TRUNCATED ISOFORM).
FT VARSPIC 521 818 MISSING (IN TRUNCATED ISOFORM).
SQ SEQUENCE 818 AA; 91736 MW; D1BA39E2092B2152 CRC64;

Query Match 13.1%; Score 648; DB 1; Length 818;
Best Local Similarity 34.2%; Pred. No. 2.3e-27;
Matches 176; Conservative 71; Mismatches 149; Indels 118; Gaps 19;

OY 446 LLSKARRVLEELTYH-LSVPDITLNNRPPREPPYOE---PRPGNPPH----- 495
DB 360 LLAKNYGEDEKRVDAHFMSVPGD-----GSGPIVDPDYVEYETTPNDGDTNNNSQI 413
OY 496 SARCVENG-----SALLSNPAYRLLATYARPP---RGSGPTPAAPAKR 537
DB 414 TSDVSNKKEHEDSTIYVVVIGIALVCTGIVMLILKFRHSKFGKGP----- 463
OY 538 TMTQAVSGDYMEPEKGPAPLPPPPNSVPHVAEDIVTLOGVTGNTYAVPALPGAVG 597
DB 464 --SSVISND--DGSASPL-----HHISNGSNPSSSEGGPDVAVIIGTKIPVI 507
OY 598 DGPPIVDFRSRRL-----FKKIEGEGFGEVHLCE---VDSQDVLVSLDF 640
DB 508 ENPQYFGITNSQLKPDTEVOHIKRNIYVKRELGEAGFVFLAECYNLCPEOD----- 561
OY 641 PLNVKRGHPLLVAKILRPDATTNKAASFSLFSRNDPLKEYVIRLDPNIRLLGVQVD 700
DB 562 -----KILVAVKTLK-DASDNA-----RKDFHEALTLNLOHEHVKYGVCEVG 606
OY 701 DPLCMITDYMENGLNQLFSAHOLEDKAAGAPDGOAAG---PTISYMLLHVAAQIA 757
DB 607 DPLIMFEYMKHGDINKFLRAH-----GPDVAVLMEGNRPAELTQGMHIAQIA 657
OY 758 SGMRVYATLAFVHRLATRNCLVGENFTIKIADFGSRNLIADYIRVOCRAVLPIRMA 817
DB 658 AAMVYLAHQFVHRLATRNCLVGENMLVKGIFGMSRDVYSTDYRYVSGHTMLPIRMP 717
OY 818 WECILGKFTTASDVAFVTLMEVLMLCRAOPGQLTDEOVLENNGEPPRDGROVYLS 877
DB 718 PPSIMKRTTSSDWSLVLMEITTYCK-QPWQLSNNEVECT-----TQGR--VLD 769
OY 878 RPPACPOGLYELMLRCMSRESEQRPFSQLHREL 911
DB 770 RPTCPKEYYDMLGCGWQREPRHRLNIKEIHSL 803

RESULT 9
TRKB_HUMAN
ID AC 016620; 016675;
STANDARD; PRT; 822 AA.

```

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DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE BDNF/NT-3 growth factors receptor precursor (EC 2.7.1.112) (TRKB
DE tyrosine kinase) (GP145-trkb) (TRK-B).
GN NTRK2 OR TRKB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_Taxid=9606;
OX [1]
PP SEQUENCE FROM N.A. (LONG FORM).
PP TISSUE-Hippocampus;
RX MEDLINE=95123473; PubMed=7823156;
RA Shelton D.L., Sutherland J., Gripp J., Camerito T., Armanini M.P.,
RA Phillips H.S., Carroll K., Spencer S.D., Levinson A.D.;
RT "Human trks: molecular cloning, tissue distribution, and expression
RT of extracellular domain immunoadhesins.";
RL J. Neurosci. 15:477-491(1995).
RN [3]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (LONG AND TRUNCATED FORMS).
RP TISSUE-Brain;
RX MEDLINE=95123473; PubMed=7823156;
RA Allen S.J., Dawbarn D., Eckford S.D., Wilcock G.K., Ashcroft M.,
RA Colebrook S.M., Feeney R., Macgowan S.H.;
RT "Cloning of a non-catalytic form of human trkb and distribution of
RT messenger RNA for trkb in human brain.";
RL Neuroscience 60:825-834(1994).
RN [1]
RP FUNCTION: RECEPTOR FOR BRAIN-DERIVED NEUROTROPHIC FACTOR (BDNF),
RP NEUROTROPHIN-3 AND NEUROTROPHIN-4/5 BUT NOT NERVE GROWTH FACTOR
RP (NGF). INVOLVED IN THE DEVELOPMENT AND/OR MAINTENANCE OF THE
RP NERVOUS SYSTEM. THIS IS A TYROSINE-PROTEIN KINASE RECEPTOR. KNOWN
RP SUBSTRATES FOR THE TRK RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-
RP GAMMA-1.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
CC tyrosine phosphate.
CC -1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
CC AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: A TRUNCATED NON-CATALYTIC FORM WHICH
CC FUNCTION REMAINS STILL UNCLEAR IS PRODUCED BY ALTERNATIVE
CC SPLICING. THE RATIO OF FULL-LENGTH TO TRUNCATED FORM IS HIGHER IN
CC FETAL THAN IN ADULT BRAIN.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED, MAINLY IN THE NERVOUS
CC TISSUE. IN THE CNS, EXPRESSION IS OBSERVED IN THE CEREBRAL CORTEX,
CC HIPPOCAMPUS, THALAMUS, CHOROID PLEXUS, GRANULAR LAYER OF THE
CC CEREBELLUM, BRAIN STEM, AND SPINAL CORD. IN THE PERIPHERAL NERVOUS
CC SYSTEM, IT IS EXPRESSED IN MANY CRANIAL GANGLIA, THE OPHTHALMIC
CC NERVE, THE VESTIBULAR SYSTEM, MULTIPLE FACIAL STRUCTURES, THE
CC SUBMAXILLARY GLANDS, AND DORSAL ROOT GANGLIA.
CC -1- PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES. TRK-TYPE SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC
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CC or send an email to license@sdb.ch).

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EMBL: U12140; AAC51371.1; -
 DR EMBL: S76473; AAB33109.1; -
 DR EMBL: S76474; AAB33110.1; -
 DR EMBL: X75958; CAAS3571.1; -
 DR HSSP: P11362; IAGW.
 DR MIM: 600456; -
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003598; Ig_c2.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_cterm.
 DR InterPro: IPR000372; LRR_Nterm.
 DR InterPro: IPR002011; Receptor_Tyr_Kin_II.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00047; Ig_1.
 DR Pfam: PF00560; LRR_1.
 DR Pfam: PF01463; LRRCT_1.
 DR Pfam: PF01462; LRRNT_1.
 DR Pfam: PF00069; pkinase_1.
 DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00408; IGC2_1.
 DR SMART: SM00082; LRRCT_1.
 DR SMART: SM00013; LRRNT_1.
 DR SMART: SM00219; TYKC_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
 DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM_1.
 DR Transferrase: Tyrosine-protein kinase; Transmembrane; ATP-binding;
 KW Phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;
 KW Leucine-rich repeat; Repeat; Immunoglobulin domain;
 KW Alternative splicing; Polymorphism.
 FT SIGNAL 1 31
 FT CHAIN 32 822
 FT DOMAIN 32 430
 FT TRANSMEM 431 454
 FT DOMAIN 455 822
 FT REPEAT 72 93
 FT REPEAT 96 117
 FT DOMAIN 214 270
 FT DOMAIN 301 365
 FT DOMAIN 338 807
 FT NP_BIND 544 552
 FT BINDING 572 572
 FT ACT_SITE 516 516
 FT MOD_RES 702 702
 FT MOD_RES 706 706
 FT MOD_RES 707 707
 FT MOD_RES 817 817
 FT SITE 516 516
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 FT SITE 817 817
 FT CARBOHYD 67 67
 FT CARBOHYD 95 95
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 FT CARBOHYD 178 178
 FT CARBOHYD 205 205
 FT CARBOHYD 241 241
 FT CARBOHYD 254 254
 FT CARBOHYD 280 280
 FT CARBOHYD 325 325
 FT CARBOHYD 338 338
 FT CARBOHYD 412 412
 FT CARBOHYD 467 477
 FT VARSPIC 478 822
 FT VARIANT 338 338
 FT SEQUENCE 822 AA; 91998 MW; 2FEB9159948FDD13 CRC64;

Query Match 13.1%; Score 645; DB 1; Length 822;
 Best Local Similarity 46.5%; Pred. No. 3,3e-27;
 Matches 144; Conservative 45; Mismatches 79; Indels 42; Gaps 10;
 QY 607 RSRTRKKEKLGSGQFGEVNLCE---VDSPODLVSLDFPLNVRKGHLYAVVITLRDARK 663
 DB 535 RSNIVAKRELGEAGFAGKVFLEECYNLCPPD-----KILVAVFTLK-DASD 579
 QY 664 NASFSLEFSRNDLFKEVKISRLKDPNIIRLGLGVQVDDPLCMITDMENGDLNFOFLSAHQ 723
 DB 580 NA-----KRDHREBELLTNLQHEIIVAFYGVGVGDELINFEFMKGGDLNKFIRABG 633
 QY 724 LED-KAEGAPDGGQAAGPT-ISYPMLLHVAQAISGMRKYATLNFVRDLATRNCLVG 781
 DB 634 PDAVLAAEGNP-----PTELQSQMHLIAQAIAGVYLLASQFVRDLATRNCLVG 685
 QY 782 ENFTIKIADFGMSRLNIYADYIRVQGRAVLPFRMAAMECLMGKFTTASDVAFGYTLNE 841
 DB 686 ENLIVKIGDFGMSRDYVSYDYRVGHTMLPIRMMPESIMYRKFTTESDVSLGVVME 745
 QY 842 VMLCRAOPFGQITDQVTEENAGEFRDQROVYLSRPPACPGYLEMLRCMSRESROR 901
 DB 746 IFTYGR-QPWYQDSNNEVEICT-----TQGR-VLQRPRTCPQVEYELMLGCMQRPENR 797
 QY 902 PPSQLRFL 911
 DB 798 KNKKGHTLL 807

RESULT 10
 ID TRKA_HUMAN STANDARD; PRT; 796 AA.
 AC P04629; P08119; Q9U107;
 DT 13-AUG-1987 (rel. 05; Created)
 DT 15-JUL-1998 (rel. 36; Last sequence update)
 DT 16-OCT-2001 (rel. 40; Last annotation update)
 DE High affinity nerve growth factor receptor precursor (EC 2.7.1.112)
 DE (TRK1 transforming tyrosine kinase protein) (p140-TrkA) (Trk-A).
 GN NTRK1 OR TRK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (TRKA-I ISOFORM).
 RC TISSUE=Colon.
 RX MEDLINE=89181575; PubMed=2927393;
 RA Martin-Zanca D., Oskam R., Mitra G., Copeland T.D., Barbacid M.;
 RT "Molecular and biochemical characterization of the human trk proto-
 oncogene.";
 RL Mol. Cell. Biol. 9:24-33(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95123473; PubMed=7823156;
 RA Shelton D.L., Sutherland J., Gripp J., Camerato T., Armanini M.P.,
 RA Phillips H.S., Carroll K., Spencer S.D., Levinson A.D.;
 RT "Human trks: molecular cloning, tissue distribution, and expression
 of extracellular domain immunoadhesins.";
 RL J. Neurosci. 15:477-491(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97435581; PubMed=9290260;
 RA Indo Y., Mardy S., Tsuneta M., Katim M.A., Matsuda I.;
 RT "Structure and organization of the human TRKA gene encoding a high
 affinity receptor for nerve growth factor.";
 RL Jpn. J. Hum. Genet. 42:343-351(1997).
 RN [4]
 RP SEQUENCE OF 399-796 FROM N.A.
 RX MEDLINE=86146854; PubMed=2869410;
 RA Martin-Zanca D., Hughes S.H., Barbacid M.;
 RT "A human oncogene formed by the fusion of truncated tropomyosin and
 protein tyrosine kinase sequences.";

RL Nature 319:743-748(1986).
RN (5)
RP SEQUENCE OF 399-796 FROM N.A.
RX MEDLINE-88196074; PubMed-2966065;
RA Kozma S.C., Redmond S.M.S., Saurer S.M., Groner B., Hynes N.E.;
RT "Activation of the receptor kinase domain of the trk oncogene by
RT recombination with two different cellular sequences.";
RL EMO J. 7:147-154(1988).
RN (6)
RP FUNCTION.
RX MEDLINE-91218846; PubMed-1850821;
RA Hemstead B.L., Martin-Ganca D., Kaplan D.R., Parada L.F., Chao M.V.;
RT "High-affinity NGF binding requires coexpression of the trk proto-
RT oncogene and the low-affinity NGF receptor.";
RL Nature 350:678-683(1991).
RN (7)
RP FUNCTION.
RX MEDLINE-91191557; PubMed-1849459;
RA Klein R., Jing S., Nanduri V., O'Rourke E., Barbacid M.;
RT "The trk proto-oncogene encodes a receptor for nerve growth factor.";
RL Cell 65:189-197(1991).
RN (8)
RP ALTERNATIVE SPLICING.
RX MEDLINE-93315496; PubMed-8325889;
RA Barker P.A., Lomen-Hoerth C., Gensch E.M., Meakin S.O., Glass D.J.,
RT Shooter E.M.;
RL "Tissue-specific alternative splicing generates two isoforms of the
RL trkA receptor.";
RL J. Biol. Chem. 268:15150-15157(1993).
RN (9)
RP MUTAGENESIS OF TYR-791.
RX MEDLINE-94179299; PubMed-7510697;
RA Loeb D.M., Stephens R.M., Copeland T.D., Kaplan D.R., Greene L.A.;
RT "A trk nerve growth factor (NGF) receptor point mutation affecting
RT interaction with phospholipase C-gamma 1 abolishes NGF-promoted
RT peripheral induction but not neurite outgrowth.";
RL J. Biol. Chem. 269:8901-8910(1994).
RN (10)
RP MUTAGENESIS, AND PHOSPHORYLATION SITES.
RX MEDLINE-94206546; PubMed-8155326;
RA Stephens R.M., Loeb D.M., Copeland T.D., Pawson T., Greene L.A.,
RT Kaplan D.R.;
RL "Trk receptors use redundant signal transduction pathways involving
RL SHC and PLC-gamma 1 to mediate NGF responses.";
RL Neuron 12:691-705(1994).
RN (11)
RP STRUCTURE BY NMR OF 489-500.
RX MEDLINE-96097066; PubMed-8524391;
RA Zhou M.M., Ravichandran K.S., Olejniczak E.F., Petros A.M.,
RA Meadows R.P., Sattler M., Hailan J.E., Wade W.S., Burakoff S.J.,
RA Feak S.W.;
RT "Structure and ligand recognition of the phosphorylase binding
RT domain of Shc.";
RL Nature 378:584-592(1995).
RN (12)
RP VARIANT CIPA ARG-577.
RX MEDLINE-96331294; PubMed-8696348;
RA Indo Y., Tsutsumi M., Hayashida Y., Karim M.A., Ohta K., Kawano T.,
RA Mitsubuchi H., Tonoki H., Aways Y., Matsuda I.;
RT "Mutations in the TRKA/NGF receptor gene in patients with congenital
RT insensitivity to pain with anhidrosis.";
RL Nat. Genet. 13:485-488(1996).
RN (13)
RP VARIANT CIPA PRO-780.
RX MEDLINE-99192367; PubMed-10090906;
RA Greco A., Villa R., Tupino B., Romano L., Pienotti M.A.;
RT "A Novel NTRK1 Mutation Associated with Congenital Insensitivity to
RT Pain with Anhidrosis.";
RL Am. J. Hum. Genet. 64:1207-1210(1999).
RN (14)
RP VARIANTS CIPA P-213; W-649 AND S-714, AND VARIANTS S-85; Y-604 AND
RP V-613.
RX MEDLINE-99264238; PubMed-10330344;

RA Mardy S., Mura Y., Endo F., Matsuda I., Sztrika L., Frossard P.,
RA Moosa A., Ismail E.A.R., Macaya A., Andria G., Toscano E., Gibson W.,
RA Graham G.E., Indo Y.;
RT "Congenital insensitivity to pain with anhidrosis: novel mutations in
RT the TRKA (NTRK1) gene encoding a high-affinity receptor for nerve
RT growth factor.";
RL Am. J. Hum. Genet. 64:1570-1579(1999).
RN (15)
RP VARIANTS TYR-604; VAL-613 AND GLN-780.
RX MEDLINE-99371280; PubMed-10443680;
RA Glimm O., Greco A., Hoang-Vu C., Dralle H., Pierotti M.A., Eng C.;
RT "Mutation analysis reveals novel sequence variants in NTRK1 in
RT sporadic human medullary thyroid carcinoma.";
RL J. Clin. Endocrinol. Metab. 84:2784-2787(1999).
RN (16)
RP VARIANT CIPA VAL-587.
RX MEDLINE-99250414; PubMed-10233776;
RA Yotsunoto S., Setoyama M., Hozumi H., Mizoguchi S., Fukumaru S.,
RA Kobayashi K., Saheki T., Kanazaki T.;
RT "A novel point mutation affecting the tyrosine kinase domain of the
RT TRKA gene in a family with congenital insensitivity to pain with
RT anhidrosis.";
RL J. Invest. Dermatol. 112:810-814(1999).
RN (17)
RP VARIANT CIPA LEU-695, AND VARIANT VAL-613.
RX MEDLINE-20321341; PubMed-10861667;
RA Shatzky S., Moses S., Levy J., Plinsk V., Hershkovitz E., Herzog L.,
RA Shorer Z., Luder A., Patvari R.;
RT "Congenital insensitivity to pain with anhidrosis (CIPA) in
RT Israeli-Bedouins: genetic heterogeneity, novel mutations in the
RT TRKA/NGF receptor gene, clinical findings, and results of nerve
RT conduction studies.";
RL Am. J. Med. Genet. 92:353-360(2000).
RN (18)
RP VARIANTS CIPA PRO-93; ARG-522; ARG-577; CYS-654 AND TYR-674.
RX MEDLINE-20435070; PubMed-10982191;
RA Mura Y., Mardy S., Aways Y., Nibel K., Endo F., Matsuda I., Indo Y.;
RT "Mutation and polymorphism analysis of the TRKA (NTRK1) gene encoding
RT a high-affinity receptor for nerve growth factor in congenital
RT insensitivity to pain with anhidrosis (CIPA) families.";
RL Hum. Genet. 106:116-124(2000).
RN (19)
RP VARIANT CIPA ARG-577.
RX MEDLINE-20036616; PubMed-10567924;
RA Greco A., Villa R., Fusetti L., Orlandi R., Pierotti M.A.;
RT "The Gly571Arg mutation, associated with the autonomic and sensory
RT disorder congenital insensitivity to pain with anhidrosis, causes the
RT inactivation of the NTRK1/nerve growth factor receptor.";
RL J. Cell. Physiol. 182:127-133(2000).
RN (20)
RP FUNCTION: REQUIRED FOR HIGH-AFFINITY BINDING TO NERVE GROWTH
RP FACTOR (NGF), NEUROKININ-3 AND NEUROKININ-4/5 BUT NOT BRAIN-
RP DERIVED NEUROTROPHIC FACTOR (BDNF). KNOWN SUBSTRATES FOR THE TRK
RP RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-GAMMA-1. HAS A CRUCIAL
RP ROLE IN THE DEVELOPMENT AND FUNCTION OF THE NOCICEPTIVE RECEPTION
RP SYSTEM AS WELL AS ESTABLISHMENT OF THERMAL REGULATION VIA
RP SWEATING. ACTIVATES ERK1 BY EITHER SHC- OR PLC-GAMMA-1-DEPENDENT
RP SIGNALING PATHWAY.
RN (21)
RP CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
RP tyrosine phosphate.
RN (22)
RP SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
RP AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES.
RN (23)
RP SUBCELLULAR LOCATION: Type I membrane protein.
RN (24)
RP ALTERNATIVE PRODUCTS: 2 ISOFORMS, TRKA-I AND TRKA-II (SHOWN
RP HERE). ARE PRODUCED BY ALTERNATIVE SPLICING. BOTH ISOFORMS HAVE
RP SIMILAR BIOLOGICAL PROPERTIES.
RN (25)
RP TISSUE SPECIFICITY: TRKA-II IS PRIMARILY EXPRESSED IN NEURONAL
RP CELLS; TRKA-I IS FOUND IN NON-NEURONAL TISSUES.
RN (26)
RP PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.
RN (27)
RP DISEASE: THE AMINO END OF SEVERAL DIFFERENT CELLULAR PROTEINS
RP (SUCH AS NON-MUSCLE TROPOMYOSIN TM30NM) HAS BEEN FOUND FUSED WITH
RP THE PROTEIN TYROSINE KINASE DOMAIN ENCODED BY NTRK1. THESE SOMATIC
RP REARRANGEMENT CREATES AN ONCOGENIC PROTEIN.
CC

CC -1- DISEASE: DEFECTS IN NTRK1 ARE A CAUSE OF A DISEASE CALLED CIPA;
 CC WHICH IS CHARACTERIZED BY A CONGENITAL INSENSITIVITY TO PAIN,
 CC ANHIDROSIS (ABSENCE OF SWEATING), ABSENCE OF REACTION TO NOXIOUS
 CC STIMULI, SELF-MUTILATING BEHAVIOR, AND MENTAL RETARDATION. THIS
 CC RARE AUTOSOMAL RECESSIVE DISORDER IS ALSO KNOWN AS CONGENITAL
 CC SENSORI NEUROPATHY WITH ANHIDROSIS OR HEREDITARY SENSORY AND
 CC AUTONOMIC NEUROPATHY TYPE IV OR FAMILIAL DYSAUTONOMIA TYPE II.
 CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES. TRK-TYPE SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

Query Match 13.0%; Score 642; DB 1; Length 796;
 Best Local Similarity 28.6%; Pred. No. 4,5e-27;
 Matches 230; Conservative 87; Mismatches 245; Indels 242; Gaps 32;

QY 238 LDFRKSQELR---VWPQDYVGSNHSFSGYVEKEFEFRLR-----AFQAM 283
 DB 84 LRLRLGELRLNLTIVKSGRLFAVAPDAFHTPLRLNLSFNALSLSMKTVQGLSLQEL 143
 QY 284 OVHONNMHTLGARLPGVEGRFRGRPAMWGE-----PMRNLGSGNLG 327
 DB 144 VLSGNPLH-----CSCALRW--LQWKEBGLGVPEQKLOCHGQGLAHMPNASC 192
 QY 328 DPRARA---VSYPLGGRVAFRLQC---RFLFAGPWLLESEISFISDVYNNSSPALGT 379
 DB 193 VPLTKGVNPAASVDYGDV---LLRCQVEGRGLQAGWIL----- 229
 QY 380 FPPAPMPPEPPPPNSSLLEPRGQOPVAKAGSPTALLIGLVALILLILLITALLML 439
 DB 230 -----TELEQ--SATYAKSGGLPS-----LGLTLAVNTS 256
 QY 440 RLHWRLLSKARVYLEELTLHLSV--PGDTLL-----INNRGPR--- 479
 DB 257 DLNKKNLTCMAENDVGAELSVQVNSFASVQHLTAVERNHCIPRSVDGQAPSLRL 316
 QY 480 -----EPPPYDEPR---PRGNPRHAPCVNGS--ALLLSNP---AYR 514
 DB 317 FNGSVLNETSFITFLEPRANETVRHGLRLNQPTH---VANGNTLLAANPFGASA 372
 QY 515 LLLATYARPP--RGPPPTPAMAKPTNTQAYSGDYNE--PEKP----- 553
 DB 373 SIMAAFNDNFEPENPEPDPVSEFSDVNTSGDPVEKDETFPGYSVAVGLAVFACFL 432
 QY 554 -----GAPLLRPPQNSVPHYAADIYVLQVGTGNTYAVPALRP 593
 DB 433 STILLVLNKCGRNKKGINRPVALAPEDGLAMSLHF---MTLGGSSLSPTGKSGSLQ 487
 QY 594 GAVGDDPPRVD-----FPRSRLRFKEKLGEGFGEVHLCEVDS---PODLVSLDFPLNV 644
 DB 488 GHITENQVYSDACVNHKIKRODIVLAKWELGEGAFKVFPLAECHNLBEO----- 537
 QY 645 RKCHPLLVAVKILRPDAKNAFSLFSRNDELKVKIMSKLPDNTIRLIGVCVODPLC 704
 DB 538 -----KMLVAVK-----ALKKASES--ARODFOREAEELTLMLOHNIYFRFEGVTEGRP 586
 QY 705 MTDVYENGDLNQLFSLAHOLEDKAGAPGDGAAGPTISYPMILHVAQAISGKRYLA 784
 DB 587 MVEYHGHGDLNPLFSLSHGDAKLAGE---DVAPGP--LGIGQLLAIVASQVAGWYLA 642
 QY 765 TLNFVHRLDTRNCLVGENFTIKIADFGMSRLYAGDYRVVQGRAVLPIRMAMECILL 824
 DB 643 GLHFVHRLDTRNCLVGGGLVYIGDFGMSRDISTDYRVGGRITMLPIRMMPESILVR 702
 QY 825 KFTTASDVAFVCTLTLEVMILCAQPPGGLTDQVLENNAGEFPDQGRQVYLSRPACQ 884
 DB 703 KFTTEDVAFSGVLTLEIFYFGK--QPMYOLISNTEAIDCI-----TOGRE--LERPRAC 754
 QY 885 GLYELMLRCMSRESEORPPSOLH 908
 DB 755 EYVAIRMGCKQRPQQRHSHKIDVH 778

RESULT 11

TRKA_RAT	STANDARD;	PRT;	799 AA.
AC	P53739;		
DT	01-JUN-1994 (Rel. 29, Created)		
DT	01-JUN-1994 (Rel. 29, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	High affinity nerve growth factor receptor precursor (EC 2.7.1.112)		
DE	(p140-TRKA) (Slow nerve growth factor receptor) (Trk-A).		
GN	NTRK1 OR TRKA OR TRK.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NBLTaxid-10116;		
RN	[1]		
RP	SEQUENCE FROM N.A. (TRKA-II ISOFORM).		
RX	MEDLINE-92196121; PubMed-1312719;		
RA	Meakin S.O., Suter U., Drinkwater C.C., Welcher A.A., Shooter E.M.,		
RT	"The rat trk protooncogene product exhibits properties characteristic		
RT	of the slow nerve growth factor receptor."		
RL	Proc. Natl. Acad. Sci. U.S.A. 89:2374-2378(1992).		
RN	[2]		
RP	ALTERNATIVE SPLICING.		
RX	MEDLINE-93315496; PubMed-8325889;		
RA	Barker P.A., Lomen-Hoerth C., Gensch E.M., Meakin S.O., Glass D.J.,		
RT	Shooter E.M.,		
RT	"Tissue-specific alternative splicing generates two isoforms of the		
RL	trkA receptor."		
RL	J. Biol. Chem. 268:15150-15157(1993).		
CC	-1- FUNCTION: REQUIRED FOR HIGH-AFFINITY BINDING TO NERVE GROWTH		
CC	FACTOR (NGF), NEUROTROPHIN-3 AND NEUROTROPHIN-4/5 BUT NOT BRAIN-		
CC	DERIVED NEUROTROPHIC FACTOR (BDNF). KNOWN SUBSTRATES FOR THE TRK		
CC	RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-GAMMA-1. HAS A CRUCIAL		
CC	ROLE IN THE DEVELOPMENT AND FUNCTION OF THE NOCICEPTIVE RECEPTION		
CC	SYSTEM AS WELL AS ESTABLISHMENT OF THERMAL REGULATION VIA		
CC	SWEATING. ACTIVATES ERK1 BY EITHER SHC OR PLC-GAMMA-1-DEPENDENT		
CC	SIGNALING PATHWAY (BY SIMILARITY).		
CC	-1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein		
CC	tyrosine phosphate.		
CC	-1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW		
CC	AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES.		
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.		
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: TRKA-I AND TRKA-II (SHOWN		
CC	HERE); ARE PRODUCED BY ALTERNATIVE SPLICING. BOTH ISOFORMS HAVE		
CC	SIMILAR BIOLOGICAL PROPERTIES.		
CC	-1- TISSUE SPECIFICITY: TRKA-II IS PRIMARILY EXPRESSED IN NEURONAL		
CC	CELLS; TRKA-I IS FOUND IN NON-NEURONAL TISSUES.		
CC	-1- PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.		
CC	-1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-		
CC	PROTEIN KINASES. TRK-TYPE SUBFAMILY.		
CC	-1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).		
CC	-1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.		
CC	-1- This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/		
CC	or send an email to license@sib-sib.ch).		
CC	-----		
DR	EMBL: M85214; AAA2286.1; -		
DR	EMBL: L12225; -; NOT_ANNOTATED_CDS.		
DR	PIR: A41981; TVRTB.		
DR	HSSP: P11362; IYGR.		
DR	Interpro: IPR000719; Euk_pkinase.		
DR	Interpro: IPR003599; IG.		
DR	Interpro: IPR001611; LRR.		
DR	Interpro: IPR000483; LRR_Cterm.		
DR	Interpro: IPR002011; Receptor_Tyr_kin_II.		
DR	Interpro: IPR001245; Tyr_pkinase.		
DR	Pfam: PF00560; LRR; 2.		

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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X93581; CA63785.1; -
 DR HSP, P11362; IREG.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003006; Ig_2MC.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR002011; Receptor_Tyr_Kin_II.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00047; Ig_1.
 DR Pfam: PF01463; LRR; 2.
 DR Pfam: PF00063; pkinase; 1.
 DR SMART; SM00409; Ig; 1.
 DR SMART; SM00082; LRCT; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
 DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Leucine-rich repeat;
 KW Immunoglobulin domain; Neurogenesis; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 14
 FT CHAIN 15 778
 FT DOMAIN 15 400
 FT TRANSSEM 401 421
 FT DOMAIN 422 778
 FT REPEAT 69 92
 FT REPEAT 94 116
 FT DOMAIN 193 250
 FT DOMAIN 281 347
 FT DOMAIN 493 763
 FT NP_BIND 499 507
 FT BINDING 527 527
 FT ACT_SITE 633 633
 FT MOD_RES 479 479
 FT MOD_RES 659 659
 FT MOD_RES 663 663
 FT MOD_RES 664 664
 FT MOD_RES 773 773
 FT SITE 479 479
 FT SITE 773 773
 FT CARBOHYD 100 100
 FT CARBOHYD 130 130
 FT CARBOHYD 143 143
 FT CARBOHYD 151 151
 FT CARBOHYD 194 194
 FT CARBOHYD 234 234
 FT CARBOHYD 262 262
 FT CARBOHYD 300 300
 FT CARBOHYD 320 320
 FT CARBOHYD 340 340
 FT CARBOHYD 384 384
 FT SEQUENCE 778 AA; 87338 MW; 4B30CDD289A3C300 CRC64;
 Query Match 12.98; Score 636.5; DB 1; Length 778;
 Best Local Similarity 31.28; Pred. No. 8.7e-27;
 Matches 196; Conservative 75; Mismatches 176; Indels 181; Gaps 24;
 OY 356 WLSESEISFDVYNNSSPLGCTFPAPMPPPTNTSSLELEPGQGPVAKAGSCP 415
 DB 226 WEVLVEINNISSILNHR-----DLTCAENSGLAEDS- 258

OY 416 TAILIGCVAILLILILILALMLRLHWR-----RLLSKAERRLVEELVHLVSY--- 465
 DB 259 -VMLNVTTPPYILLISEAIPQHFICIPFSVDSNPPLRLMLFNGSKLDEGPYIRIRVEY 317
 OY 466 -PGDTILIN---NRGPREPPPYOEPRRGNPPHSACVPNGS-ALLSNPAVRLIAT 519
 DB 318 EPNSTVLHGCIQLNR-----PTH-----VANGNTLVAVNP-----LGR 351
 OY 520 YARPRG-----PGPTPAMAKPTNQASGDYMEPEKPGAPLLPPPPNSVPHY 569
 DB 352 AARSIOGRFMDNPPSPSEDEPIPVISISPLGRNNS-----LEGPFVETADHT 398
 OY 570 AEADIVTLQGY-----TGNTAAYPALPG-----AVGCP 600
 DB 399 FGVSVAVALAVPASLFLSVMLIALNKGHRKFGINRSVAVLAPEDGLMSLHFMTLGSSP 458
 OY 601 -----PRVD-----PPSRRLFEKELGEGFGEVHCEYDS--PQ 633
 DB 459 VSTESKLDGLKSNFTENPQFCNACVHHVQRDVLKWELEGAFKVFPLAECSHLPE 518
 OY 634 DLVSLDFPLNKRKGPLLVAVKIIRPDATKNAFSLFSRNDPLKEVKIMSLKDPNIIRL 693
 DB 519 Q-----EKLTVAVKALK-EVTENA-----RLDFORAEELTVLQHEHIYKF 558
 OY 694 LGVCVODDPLCMITDYMNGDPLNGLFSLAHQLEDKAEGAPDGAAGPTISYPLHLVA 753
 DB 559 XGVCTEGDPLINVEYKMKHGLNRLNSHGPDAKLD--QDGGCCGLTISH--MLQIA 614
 OY 754 AQLASGRMYLATLNFVRHDLATRNCLVGENFTIKIADFGMSRNLVAGDYRVOGRVPLPI 813
 DB 615 TQISGMVYLLASLHFVHDLATRNCLVGHDLVVKIGDGMGRDLYSTGYVGGFTMLPI 674
 OY 814 RWMAMECIAMKFTTASVVAFFGVTLMVLMCRAPPGQLTDEQVYINAGEFFRDGRO 873
 DB 675 RWPMPESLTYKRTTESDSIWSFGVYLWEIIFYGK-QPWYQLSNTEALICI-----TQGRE 728
 OY 874 VYLSRPACPGLEYELMCRWRESEOR 901
 DB 729 --LRRPRCPSEVVIDIMOSCOREPOOR 754
 RESULT 13
 TRKC CHICK STANDARD; PRT; 827 AA.
 AC 091044; 092022; 091011;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE NT-3 growth factor receptor precursor (Ec 2.7.1.112) (TrkC tyrosine
 kinase) (Trk-C).
 GN TRKC.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID:9031.
 RN
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
 RC TISSUE-Embryonic Brain;
 RX MEDLINE-94338700; PubMed-8060621;
 RA Garner A.S., Large T.H.;
 RT "isoforms of the avian TrkC receptor: a novel kinase insertion
 RT dissociates transformation and process outgrowth from survival.";
 RL Neuron 13:457-472(1994).
 RN
 RN SEQUENCE FROM N.A. (ISOFORMS ALPHA/FL AND TRKC-3).
 RP MEDLINE-93359043; PubMed-8394830;
 RA Okazawa H., Kamei M., Kanazawa I.;
 RT "Molecular cloning and expression of a novel truncated form of
 RT chicken TrkC.";
 RL FEBS Lett. 329:171-177(1993).
 RN [3]

RP SEQUENCE OF 378-513 FROM N.A.
RC TISSUE-Embryo;
RA MEDLINE-94084905; PubMed-8261614;
RA Williams R., Backstrom A., Ebendal T., Hallbook F.;
RT "Molecular cloning and cellular localization of trkC in the chicken embryo";
RL Brain Res. Dev. Brain Res. 75:235-252(1993).
CC -1- FUNCTION: RECEPTOR FOR NEUROTROPHIN-3 (NT-3). THIS IS A TYROSINE-
CC PROTEIN KINASE RECEPTOR. KNOWN SUBSTRATES FOR THE TRK RECEPTORS
CC ARE SHC, PI-3 KINASE, AND PLC-GAMMA-1.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
CC tyrosine phosphate.
CC -1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
CC AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES.
CC -1- SUBCELLULAR LOCATION: TYPE I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: SEVERAL ISOFORMS ARE PRODUCED BY ALTERNATIVE
CC SPLICING GIVING RISE TO RECEPTORS WITH DISTINCT FUNCTIONAL
CC CAPABILITIES. THEY DIFFER IN THE EXTRACELLULAR MOTIF (ALPHA OR
CC BETA TYPES) AND/OR IN THE KINASE DOMAIN (KI, KD, KT, FL.
CC RESPECTIVELY FOR INSERTION, DELETION, TRUNCATION AND FULL LENGTH).
CC THE SEQUENCE SHOWN HERE IS THAT OF THE ALPHA/FULL LENGTH ISOFORM
CC (ALPHA/FL). THE COMBINATIONS ALPHA/FL, ALPHA/KD, AND BETA/KD HAVE
CC BEEN FOUND IN BRAIN OF A DAYS 13 AGED EMBRYO. THE KI AND KD
CC ISOFORMS FAIL TO STIMULATE TRANSFORMATION, PROCESS OUTGROWTH OR
CC SURVIVAL. THE KI ISOFORM EXHIBITS TYROSINE PHOSPHORYLATION IN THE
CC ABSENCE OF LIGAND AND IS UNABLE TO MEDIATE SURVIVAL OF NEURONAL
CC CELLS.
CC -1- DEVELOPMENTAL STAGE: EXPRESSION OCCURS IN THE EMBRYONAL DAY 2 (E2)
CC EMBRYO WITH INCREASING LEVELS LATER IN DEVELOPMENT. IN THE E9
CC EMBRYO HIGHEST LEVELS ARE FOUND IN BRAIN AND SPINAL CORD WITH
CC INTERMEDIATE LEVELS IN EYE, HEART, GUT AND MUSCLE. LOW LEVELS ARE
CC FOUND IN KIDNEY, LIVER, SKIN AND YOLK SAC.
CC -1- PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES. TRK-TYPE SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).
CC -1- CAUTION: THE ADDITIONAL KINASE-DELETED ISOFORM TRK-3 WHICH
CC REPLACES THE KINASE DOMAIN WITH 19 AA INSTEAD OF 39 IN THE KD
CC ISOFORM RESULTS FROM A FRAMESHIFT.
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: S74248; AAB31699.1; -
DR EMBL: X59669; CAA42202.1; -
DR EMBL: Z30091; CAA82907.1; -
DR HSSP: P11362; IEG1.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00047; Ig_1.
DR Pfam: PF00560; LRR_2.
DR Pfam: PF01463; LRRCT_1.
DR Pfam: PF01462; LRRNT_1.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00082; LRRCT_1.
DR SMART: SM00409; IG_1.
DR SMART: SM00013; LRRNT_1.
DR SMART: SM00219; TYRK; 1.
DR PROSITE: PS0107; PROTEIN_KINASE_ATP_1.
DR PROSITE: PS0109; PROTEIN_KINASE_TYR_1.

DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_1; 1.
KW Transferrase; Tyrosine-protein kinase; Transmembrane; ATP-binding;
KW Phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;
KW Leucine-rich repeat; Repeat; Alternative splicing;
KW Immunoglobulin domain.
FT STGNL 1 31
FT CHAIN 32 827
FT DOMAIN 33 430
FT TRANSMEM 431 455
FT DOMAIN 456 827
FT REPEAT 102 125
FT REPEAT 126 149
FT DOMAIN 227 288
FT DOMAIN 319 382
FT DOMAIN 540 812
FT NP_BIND 546 554
FT BINDING 574 574
FT ACT_SITE 681 681
FT MOD_RES 518 518
FT MOD_RES 707 707
FT MOD_RES 711 711
FT MOD_RES 712 712
FT MOD_RES 822 822
FT SITE 518 518
FT SITE 822 822
FT SITE 822 822
FT CARBOHYD 68 68
FT CARBOHYD 72 72
FT CARBOHYD 79 79
FT CARBOHYD 163 163
FT CARBOHYD 203 203
FT CARBOHYD 218 218
FT CARBOHYD 232 232
FT CARBOHYD 259 259
FT CARBOHYD 267 267
FT CARBOHYD 272 272
FT CARBOHYD 294 294
FT CARBOHYD 375 375
FT CARBOHYD 388 388
FT VARSPPLIC 1 98
FT VARSPPLIC 581 619
FT VARSPPLIC 620 827
FT VARSPPLIC 633 664
FT VARSPPLIC 665 827
FT VARSPPLIC 713 713
FT CONFLICT 1 39
FT CONFLICT 124 124
FT CONFLICT 378 378
FT CONFLICT 481 496
FT CONFLICT 795 795
SQ SEQUENCE 827 AA; 93180 MW; AB97373113DCB28A CRC64;
Query Match 12.7%; Score 626.5; DB 1; Length 827;
Best Local Similarity 44.7%; Pred. No. 3,1e-26;
Matches 139; Conservative 50; Mismatches 81; Indels 41; Gaps 10;
OY 607 RSRLRKEKLGSGGGEVHLCEVDYSLDFPLNVRKGGPLVYAKIIRPDAFKNS 666
DB 537 RRDIVLKRRLGEGAFGKFLACYNLS-----PTNDR---MVAAYAKL-DPT----- 580
OY 667 FSLFSRNDLKEVKIKMSRLKDNIIIRLLGVCYQDDPILITDYMGNDQFLSHQLED 726
DB 581 --LAARKDQRAELIITNLQHEHYIKFYGVCGDGPDLVWEIYMKHGLNFKLRAH----- 634

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QY 727 KAAGAGC-----DGAAGCP-TISYPMILHVAQAISGMRATLNFVHRDIATRNCLV 780
D 635 -----GPDAMILVDGCPROANGELGLSOMLHIAISOIASGMVYLAHQFVHRDIATRNCLV 689
QY 781 GENETIKIADGSMNRNAYAGYVROGAVYPIRMAMCECLMKKFTTASVAFGYTLW 840
D 690 GANLVATIGDGSMDYSDTYVGHVMTLPIKMPPESTMKRTTESDVSFVILW 749
QY 841 EVLMICRAOPGQLTDEQVIENAGEFFRDGROYLTSRPACQGLYELMJCWRSRESE 900
P 750 EIFTYGR-QPMFQSLNTEVIECI-----TQGR--VLERPRVCREYVDIMLGCNQRPQ 801
QY 901 RPPFSQHLREL 911
D 802 RLNIKEIKYKIL 812

RESULT 14
TRKC_PIG STANDARD; PRT; 825 AA.
AC P24786;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE NT-3 growth factor receptor precursor (EC 2.7.1.112) (TRKC tyrosine
kinase) (GPI45-TRKC) (Trk-C).
GN NTRK3 OR TRKC.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suis.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=91364178; PubMed=1653651;
RA Lamballe F., Klein R., Barbacid M.;
RT "TrkC, a new member of the trk family of tyrosine protein kinases, is
a receptor for neurotrophin-3."
RL Cell 66:967-979(1991).
CC -1- FUNCTION: RECEPTOR FOR NEUROTROPHIN-3 (NT-3). THIS IS A TYROSINE-
PROTEIN KINASE RECEPTOR. KNOWN SUBSTRATES FOR THE TRK RECEPTORS
ARE SHC, PI-3 KINASE, AND PLC-GAMMA-1.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
tyrosine phosphate.
CC -1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: PREFERENTIALLY IN THE BRAIN, LOW LEVELS IN THE
OVARIES.
CC -1- PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
PROTEIN KINASES. TRK-TYPE SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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or send an email to license@sdb.ch).
CC -----
DR EMBL: M80800; AAA11130.1;
DR PIR: A40026; A40026.
DR HSSP: P1362; LFCK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003589; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR000372; LRR_Nterm.

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DR InterPro: IPR002011; Receptor_tyr_kin_II.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF00560; LRR; 2.
DR Pfam: PF01463; LRRCT; 1.
DR Pfam: PF01462; LRRNT; 1.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00082; LRRCT; 1.
DR SMART: SM00082; LRRNT; 1.
DR SMART: SM00013; LRRNT; 1.
DR SMART: SM00219; TYRK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferase; Tyrosine-protein kinase; Transmembrane; ATP-binding;
KW Phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;
KW Leucine-rich repeat; Repeat; Immunoglobulin domain.
FT SIGNAL 1 31
FT CHAIN 32 825
FT DOMAIN 32 429
FT TRANSMEM 430 453
FT DOMAIN 454 825
FT REPEAT 102 125
FT REPEAT 126 149
FT DOMAIN 227 288
FT DOMAIN 319 382
FT DOMAIN 538 814
FT NE_BIND 544 552
FT BINDING 572 572
FT ACT_SITE 679 679
FT MOD_RES 516 516
FT MOD_RES 705 705
FT MOD_RES 709 709
FT MOD_RES 710 710
FT MOD_RES 820 820
FT SITE 516 516
FT SITE 820 820
FT SITE 820 820
FT CARBOHYD 68 68
FT CARBOHYD 72 72
FT CARBOHYD 79 79
FT CARBOHYD 133 133
FT CARBOHYD 163 163
FT CARBOHYD 203 203
FT CARBOHYD 232 232
FT CARBOHYD 259 259
FT CARBOHYD 267 267
FT CARBOHYD 272 272
FT CARBOHYD 294 294
FT CARBOHYD 375 375
FT CARBOHYD 388 388
SQ SEQUENCE 825 AA; 93129 MW; A3C6716B1D0D8540 CRC64;
FT SITE 820 820
FT CARBOHYD 68 68
FT CARBOHYD 72 72
FT CARBOHYD 79 79
FT CARBOHYD 133 133
FT CARBOHYD 163 163
FT CARBOHYD 203 203
FT CARBOHYD 232 232
FT CARBOHYD 259 259
FT CARBOHYD 267 267
FT CARBOHYD 272 272
FT CARBOHYD 294 294
FT CARBOHYD 375 375
FT CARBOHYD 388 388
SQ SEQUENCE 825 AA; 93129 MW; A3C6716B1D0D8540 CRC64;
Query Match 12.7%; Score 624.5; DB 1; Length 825;
Best Local Similarity 29.4%; Pred. No. 3; 9e-26;
Matches 187; Conservative 85; Mismatches 175; Indels 189; Gaps 27;
QY 309 PNAW--EEGPMKHNLSGMDPRARAVSPGLGRRVAFRLQCFRLAGWLLSELSIFS 366
D 331 PFLMLHNSQPLR-----ESKITHVEYDGEVSE--GC-----LLENKPTHYN 372
QY 367 D---VYNNSSP-----ALGTFPPAPWPPPGPPY-NFSSL-ELFPR-----GOQPAK 410
D 373 NGNYTLNRQEPGLTANQTINGHFLKEPF-----PESIDNVSYEVSPTPTVTHKPEED 428
QY 411 AGSPFAIIIGCLVAIIILLIILALMLRLHWRRLSAAERVVEELTVLSPGDGI 470
D 429 TPGVSINQGLAFACVLVLFPI-----MINKYGR-----SKFGMGPA 469

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QY 471 LINRPGPREPPYOE-----RPRGNPHSAPCVNPSALLSPNAYRLLATYA 521
 DB 470 VISGEEDSASLHNDOPHHHTLTTRAGSHSVIGMTIP-----VINPOT----- 516
 QY 522 RPRGPGPPPTAMKPTTQAYSGDYMEPEKPGAPLLPPPPONSYPHYAADIYLGCVT 581
 DB 517 -----FROGNCH-----KQDTYQHILKRDIY----- 539
 QY 582 GGNVYAVPALPFGAVGDPFPRVDFPRSRLRKEKKEGEGEVEHLCEDVSPQDVLSDLP 641
 DB 540 -----LKELEGAPFKGVFLAECYNLS-----P 562
 QY 642 LNVKGPPLVAVKILRPDANKNASFSLFRNDFLEKVKINSRLKDPNILLGVCYDOD 701
 DB 563 TKV-----MLVAVALK-DPT-----LAARKDQREAEELTNLOHEHIVKFGCGGD 611
 QY 702 PLCMITDMENGDLNOFLSAHQLEDKAEGAPG-----DGOAAGP-TISYPMILHVAQ 755
 DB 612 PLIVFEVEMKRGDLNKLFLRAH-----GPDAMILVDGPPRAKGLGSLQMHMSQ 662
 QY 756 IASGMRLATINFYHRDLATNCLVGENFTIKIADFGSNRLVAGDIYRVOGRAVLPIRW 815
 DB 663 ICSGVYIASQHFVHRDLATNCLVGANLLVKIGDFGMSRDYSTDYRYVGHTMLPIRW 722
 QY 816 MAMECIIMGKRTTASDVAVKVTLMVEMILCRAOPFGLTDEOVIENAGEFFRQGRGV 875
 DB 723 MPESIMVKRTTSDVWSGVILWEITFYTK-OPWFOLSNTEVICT-----TQGR--V 774
 QY 876 LSRRPACPOGLYELMLRCWSESEORPPFSQHLREL 911
 DB 775 LERPRVCPEYVDVLMGCMQREPORLNKEIKYIL 810

RESULT 15
 TRKC_HUMAN
 ID TRKC_HUMAN STANDARD; PRT; 839 AA.
 AC 016288; 016289; 012827;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE NT-3 growth factor receptor precursor (EC 2.7.1.112) (TrkC tyrosine kinase) (GPI45-TrkC) (Trk-C).
 GN NTRK3 OR TRKC.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=95123473; PubMed=7823156;
 RA Shelton D.L., Sutherland J., Gripp J., Camerato T., Armanini M.P., Phillips H.S., Carroll K., Spencer S.D., Levinson A.D.;
 RT "Human trks: molecular cloning, tissue distribution, and expression of extracellular domain immunoadhesins.";
 RT J. Neurosci. 15:477-491(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=95104834; PubMed=7806211;
 RA McGreggor L.M., Bayliss S.B., Griffin C.A., Hawkins A.L., Nelkin B.D.;
 RT "Molecular cloning of the cDNA for human TrkC (NTRK3), chromosomal assignment, and evidence for a splice variant.";
 RT Genomics 22:267-272(1994).
 RL -1- FUNCTION: RECEPTOR FOR NEUROTROPHIN-3 (NT-3). THIS IS A TYROSINE-PROTEIN KINASE RECEPTOR. KNOWN SUBSTRATES FOR THE TRK RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-GAMMA-1.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein tyrosine phosphate.
 CC -1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- ALTERNATIVE PRODUCTS: AT LEAST FOUR FORMS OF TRKC ARE PRODUCED BY ALTERNATIVE SPLICING. THE DIFFERENT ISOFORMS DO NOT HAVE IDENTICAL SIGNALING PROPERTIES. THE ISOFORM B IS EXPRESSED IN A RELATIVELY LARGE AMOUNT IN THE ADULT BRAIN COMPARATIVELY TO FETAL BRAIN.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED, MAINLY IN THE NERVOUS TISSUE.
 CC -1- PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.
 CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-PROTEIN KINASES. TRK-TYPE SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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 CC -----
 CC EMBL: S76475; AAB3311.1; -;
 CC EMBL: S76476; AAB3311.2.1; -;
 CC EMBL: U05012; AAB75374.1; -;
 CC HSSP: P11362; IAGW.
 CC MIM: 191316; -;
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR000372; LRR_Cterm.
 DR InterPro: IPR002011; Receptor_Tyr_kin_II.
 DR InterPro: IPR001245; Tyr_Pkinase.
 DR Pfam: PF00047; Ig_1.
 DR Pfam: PF00560; LRR_2.
 DR Pfam: PF01463; LRRCT_1.
 DR Pfam: PF01462; LRRNT_1.
 DR Pfam: PF00069; Pkinase_1.
 DR SMART: SM00409; Ig_1.
 DR SMART: SM00082; LRRCT_1.
 DR SMART: SM00013; LRRNT_1.
 DR SMART: SM00219; Tyrc_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
 DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM_1.
 KW Transferrase; Tyrosine-protein kinase; Transmembrane; ATP-binding; Phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;
 KW Leucine-rich repeat; Repeat; Alternative splicing;
 KW Immunoglobulin domain.
 FT SIGNAL 1 31
 FT CHAIN 32 839
 FT DOMAIN 32 429
 FT TRANSMEM 430 453
 FT DOMAIN 454 839
 FT REPEAT 102 125
 FT REPEAT 126 149
 FT DOMAIN 227 288
 FT DOMAIN 319 382
 FT DOMAIN 538 839
 FT NP_BIND 544 552
 FT BINDING 572 572
 FT ACT_SITE 679 679
 FT MOD_RES 516 516
 FT MOD_RES 705 705
 FT MOD_RES 709 709
 FT MOD_RES 710 710
 FT MOD_RES 834 834
 FT SITE 516 516
 FT SITE 834 834
 FT SITE 834 834
 FT CARBOHYD 72 72

NT-3 GROWTH FACTOR RECEPTOR.
 EXTRACELLULAR (POTENTIAL).
 POTENTIAL.
 CYTOPLASMIC (POTENTIAL).
 LRR 1.
 LRR 2.
 IG-LIKE C2-TYPE DOMAIN 1.
 IG-LIKE C2-TYPE DOMAIN 2.
 PROTEIN KINASE.
 ATP (BY SIMILARITY).
 APP (BY SIMILARITY).
 APP (BY SIMILARITY).
 BY SIMILARITY.
 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 PHOSPHORYLATION (BY SIMILARITY).
 INTERACTION WITH SHC PROTEIN (BY SIMILARITY).
 INTERACTION WITH PLC-GAMMA-1 (BY SIMILARITY).
 N-LINKED (GLCNAC. . .) (POTENTIAL).

